

STN

FIL MEDLINE BIOSIS EMBASE SCISEARCH CAPLUS USPATFULL PCTFULL
=> s sodium and channel and polymorphism and (hh1b or hh1?)

L1 61 SODIUM AND CHANNEL AND POLYMORPHISM AND (HH1B OR
HH1?)

=> dup rem l1

PROCESSING COMPLETED FOR L1

L2 53 DUP REM L1 (8 DUPLICATES REMOVED)

=> s l1 and py<=2002

2 FILES SEARCHED...

4 FILES SEARCHED...

L3 32 L1 AND PY<=2002

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 20:37:48 ; Search time 22471 Seconds
(without alignments)
11748.584 Million cell updates/sec

Title: US-10-077-054-1
Perfect score: 6091
Sequence: 1 gatgagaagatggcaaactt.....ggccaggacacactgaaaag 6091

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:
2: gb_htg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pat:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_sts:

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28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	6091	100.0	6091	9	AF482988	AF482988 Homo sapi
2	6079.8	99.8	8414	9	AY038064	AY038064 Homo sapi
3	6075.6	99.7	6169	9	AY148488	AY148488 Homo sapi
4	6039.6	99.2	8491	6	AX449276	AX449276 Sequence
5	6039.6	99.2	8491	6	AX741279	AX741279 Sequence
6	6039.6	99.2	8491	9	HUMHH1A	M77235 Human cardiac
7	6038	99.1	8491	6	AX449278	AX449278 Sequence
8	5993.6	98.4	6048	6	AR183727	AR183727 Sequence
9	5990.4	98.3	6048	6	AR337848	AR337848 Sequence
10	5385.4	88.4	8530	6	AX552195	AX552195 Sequence
11	5119.6	84.1	6394	4	CFA555547	AJ555547 Canis fam
12	5094	83.6	6503	4	BTA251721	AJ251721 Bos tauru
13	5014.8	82.3	7545	10	RATSCAL	M27902 Rat cardiac
14	5013.4	82.3	6458	10	MMU271477	AJ271477 Mus muscu
15	4727.6	77.6	5901	6	AX348083	AX348083 Sequence
16	4727.6	77.6	5901	10	AF353637	AF353637 Rattus no
17	2553.6	41.9	6527	6	A58859	A58859 Sequence 7
18	2553.6	41.9	6527	6	AR230064	AR230064 Sequence
19	2550.8	41.9	6524	6	A58853	A58853 Sequence 1
20	2550.8	41.9	6524	6	AR230061	AR230061 Sequence
21	2550.8	41.9	6524	6	AX710158	AX710158 Sequence
22	2550.8	41.9	6524	10	RNSNS	X92184 R.norvegicu
23	2549.6	41.9	6344	6	AR253318	AR253318 Sequence
24	2549.6	41.9	6344	6	AX252389	AX252389 Sequence
25	2549.6	41.9	6344	10	RNU53833	U53833 Rattus norv
26	2508.8	41.2	6726	4	CFU60590	U60590 Canis famil
27	2487	40.8	5874	6	AR253325	AR253325 Sequence
28	2485.4	40.8	5874	6	AX252393	AX252393 Sequence
29	2485.4	40.8	5874	6	AX710162	AX710162 Sequence
30	2485.4	40.8	5874	9	AF117907	AF117907 Homo sapi
31	2432.8	39.9	6373	6	AX252391	AX252391 Sequence
32	2432.8	39.9	6373	10	MMSNS	Y09108 M.musculus
33	2243	36.8	6007	6	AR181336	AR181336 Sequence

34	2243	36.8	6586	10	AF049240	AF049240 Rattus no
35	2225.4	36.5	6586	6	AR181360	AR181360 Sequence
36	2221.6	36.5	7052	6	A58857	A58857 Sequence 5
37	2221.6	36.5	7052	6	AR230063	AR230063 Sequence
38	2214.4	36.4	5977	6	AR181335	AR181335 Sequence
39	2214.4	36.4	6556	6	AR181338	AR181338 Sequence
40	2214.4	36.4	6556	10	AF049239	AF049239 Rattus no
41	2204.2	36.2	5937	10	AF049617	AF049617 Mus muscu
42	2167.4	35.6	6826	6	AR181339	AR181339 Sequence
43	2167.4	35.6	6826	10	RATSCP6A	L39018 Rattus norv
44	2098.6	34.5	7008	6	AX741281	AX741281 Sequence
45	2098.6	34.5	7008	9	AB027567	AB027567 Homo sapi